



PF-0027 US

SUBSTITUTE SHEET

TECH CENTER 1600/2900

JUL 31 2001

RECEIVED

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Coleman, Roger
Bandman, Olga
Wilde, Craig G.
- (ii) TITLE OF THE INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: U.S.
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/390,740
 - (B) FILING DATE: February 17, 1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Luther, Barbara J.
 - (B) REGISTRATION NUMBER: 33,954
 - (C) REFERENCE/DOCKET NUMBER: PF-0027 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human Pancreas
(B) CLONE: 223187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAGGTCT	CCGCAGCACT	TCTGTGGCTG	CTGCTCATAG	CAGCTGCCTT	CAGCCCCCAG	60
GGGCTCACTG	GGCCAGCTTC	TGTCCCAACC	ACCTGCTGCT	TTAACCTGGC	CAATAGGAAG	120
ATACCCCTTC	AGCGACTAGA	GAGCTACAGG	AGAATCACCA	GTGGCAAATG	TCCCCAGAAA	180
GCTGTGATCT	TCAAGACCAA	ACTGGCCAAG	GATATCTGTG	CCGACCCCAA	GAAGAAGTGG	240
GTGCAGGATT	CCATGAAGTA	TCTGGACCAA	AAATCTCCAA	CTCCAAAGCCA		291

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human Pancreas
(B) CLONE: 223187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Val	Ser	Ala	Ala	Leu	Leu	Trp	Leu	Leu	Ile	Ala	Ala	Ala	1	5	10	15	
Phe	Ser	Pro	Gln	Gly	Leu	Thr	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys	20	25	30	
Cys	Phe	Asn	Leu	Ala	Asn	Arg	Lys	Ile	Pro	Leu	Gln	Arg	Leu	Glu	Ser	35	40	45	
Tyr	Arg	Arg	Ile	Thr	Ser	Gly	Lys	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	50	55	60	
Lys	Thr	Lys	Leu	Ala	Lys	Asp	Ile	Cys	Ala	Asp	Pro	Lys	Lys	Lys	Trp	65	70	75	80
Val	Gln	Asp	Ser	Met	Lys	Tyr	Leu	Asp	Gln	Lys	Ser	Pro	Thr	Pro	Lys	85	90	95	
Pro																			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Human Pancreas

(B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCTCAGT	CACTGGCTCT	GAGCCTCCTT	ATCCTGGTTC	TGGCCTTTGG	CATCCCCAGG	60
ACCCAAGGCA	GTGATGGAGG	GGCTCAGGAC	TGTTGCCTCA	AGTACAGCCA	AAGGAAGATT	120
CCCGCCAAGG	TTGTCCGCAG	CTACCGGAAG	CAGGAACCAA	GCTTAGGCTG	CTCCATCCCA	180
GCTATCCTGT	TCTTGCCCCG	CAAGCGCTCT	CAGGCAGAGC	TATGTGCAGA	CCCAAAGGAG	240
CTCTGGGTGC	AGCAGCTGAT	GCAGCATCTG	GACAAGACAC	CATCCCCACA	GAAACCAGCC	300
CAGGGCTGCA	GGAAGGACAG	GGGGGCCTCC	AAGACTGGCA	AGAAAGGAAA	GGGCTCCAAA	360
GGCTGCAAGA	GGACTGAGCG	GTACAGACC	CCTAAAGGGC	CA		402

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Human Pancreas

(B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Gln	Ser	Leu	Ala	Leu	Ser	Leu	Leu	Ile	Leu	Val	Leu	Ala	Phe
1				5				10					15		
Gly	Ile	Pro	Arg	Thr	Gln	Gly	Ser	Asp	Gly	Gly	Ala	Gln	Asp	Cys	Cys
			20					25					30		
Leu	Lys	Tyr	Ser	Gln	Arg	Lys	Ile	Pro	Ala	Lys	Val	Val	Arg	Ser	Tyr
		35				40						45			
Arg	Lys	Gln	Glu	Pro	Ser	Leu	Gly	Cys	Ser	Ile	Pro	Ala	Ile	Leu	Phe
	50					55					60				
Leu	Pro	Arg	Lys	Arg	Ser	Gln	Ala	Glu	Leu	Cys	Ala	Asp	Pro	Lys	Glu
65				70					75						80
Leu	Trp	Val	Gln	Gln	Leu	Met	Gln	His	Leu	Asp	Lys	Thr	Pro	Ser	Pro
			85					90						95	
Gln	Lys	Pro	Ala	Gln	Gly	Cys	Arg	Lys	Asp	Arg	Gly	Ala	Ser	Lys	Thr
			100					105						110	

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
 115 120 125
 Gln Thr Pro Lys Gly Pro
 130

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Val Ser Ala Ala Leu Leu Ala Leu Leu Leu Ile Ala Ala Ala
 1 5 10 15
 Phe Cys Pro Gln Gly Leu Ala Gln Pro Asp Gly Val Asp Thr Pro Thr
 20 25 30
 Thr Cys Cys Phe Asn Tyr Ile Asn Arg Lys Ile Pro Arg Gln Arg Leu
 35 40 45
 Glu Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Ser Lys Pro Ala Val
 50 55 60
 Ile Phe Lys Thr Lys Arg Ala Lys Gln Val Cys Ala Asp Pro Lys Glu
 65 70 75 80
 Lys Trp Val Gln Asp Ser Met Lys His Leu Asp Lys Gln Thr Pro Lys
 85 90 95
 Pro

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MIP-1a

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
 1 5 10 15

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Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
      20                      25                      30
Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
      35                      40                      45
Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
      50                      55                      60
Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
65                      70                      75                      80
Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
      85                      90

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MIP-1b

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
 1                      5                      10                      15
Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
      20                      25                      30
Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
      35                      40                      45
Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
      50                      55                      60
Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser
65                      70                      75                      80
Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
      85                      90

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: RANTES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Lys	Val	Ser	Ala	Ala	Arg	Leu	Ala	Val	Ile	Leu	Ile	Ala	Thr	Ala			
1				5					10					15				
Leu	Cys	Ala	Pro	Ala	Ser	Ala	Ser	Pro	Tyr	Ser	Ser	Asp	Thr	Thr	Pro			
			20					25					30					
Cys	Cys	Phe	Ala	Tyr	Ile	Ala	Arg	Pro	Leu	Pro	Arg	Ala	His	Ile	Lys			
		35					40					45						
Glu	Tyr	Phe	Tyr	Thr	Ser	Gly	Lys	Cys	Ser	Asn	Pro	Ala	Val	Val	Phe			
		50				55				60								
Val	Thr	Arg	Lys	Asn	Arg	Gln	Val	Cys	Ala	Asn	Pro	Glu	Lys	Lys	Trp			
65					70				75						80			
Val	Arg	Glu	Tyr	Ile	Asn	Ser	Leu	Glu	Met	Ser								
				85				90										

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: MCP-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Lys	Val	Ser	Ala	Ala	Leu	Leu	Cys	Leu	Leu	Ile	Ala	Ala	Thr				
1				5				10					15					
Phe	Ile	Pro	Gln	Gly	Leu	Ala	Gln	Pro	Asp	Ala	Ile	Asn	Ala	Pro	Val			
			20					25				30						
Thr	Cys	Cys	Tyr	Asn	Phe	Thr	Asn	Arg	Lys	Ile	Ser	Val	Gln	Arg	Leu			
		35					40					45						
Ala	Ser	Tyr	Arg	Arg	Ile	Thr	Ser	Ser	Lys	Cys	Pro	Lys	Glu	Ala	Val			
		50				55				60								
Ile	Phe	Lys	Thr	Ile	Val	Ala	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Lys	Gln			
65					70				75						80			

Pro Lys Thr

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
(B) CLONE: MCP-2

Ala	Gln	Pro	Asp	Ser	Val	Ser	Ile	Pro	Ile	Thr	Cys	Cys	Phe	Asn	Val
1				5					10					15	
Ile	Asn	Arg	Lys	Ile	Pro	Ile	Gln	Arg	Leu	Glu	Ser	Tyr	Thr	Arg	Ile
			20				25						30		
Thr	Asn	Ile	Gln	Cys	Pro	Lys	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Arg
		35				40						45			
Gly	Lys	Glu	Val	Cys	Ala	Asp	Pro	Lys	Glu	Arg	Trp	Val	Arg	Asp	Ser
	50				55					60					
Met	Lys	His	Leu	Asp	Gln	Ile	Phe	Gln	Asn	Leu	Lys	Pro			
65					70				75						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
(B) CLONE: MCP-3

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Trp	Lys	Pro	Met	Pro	Ser	Pro	Ser	Asn	Met	Lys	Ala	Ser	Ala	Ala
1				5					10					15	
Leu	Leu	Cys	Leu	Leu	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Gln	Gly	Leu	
			20				25					30			
Ala	Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe
		35					40					45			
Ile	Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr
	50					55					60				
Thr	Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu
65					70					75					80
Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe
				85					90					95	
Met	Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu			
			100					105							